SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN DISEASES

This application is a nonprovisional of U.S. provisional application Ser. No. 60/267,422, filed February 9, 2001, which is hereby incorporated by reference in its entirety. All patent and nonpatent references cited in that application, or in the present application, are also hereby incorporated by reference in their entirety. Similarly the Danish patent application Ser. No. 2001 00218, filed February 9, 2001, is hereby incorporated by reference in its entirety. All patent and nonpatent references cited in Danish patent application Ser. No. 2001 00218, are also hereby incorporated by reference in their entirety.

FIELD OF INVENTION

The present invention relates to transgenic *scce* mammals and mammalian embryos, their use as models of studying human diseases, to methods of using these models for identifying compounds and compositions effective for the treatment of these diseases, and to the compounds and compositions themselves. In particular, the invention relates to transgenic mammals overexpressing a *scce* gene in the skin. These model animals display a major change in phenotype characterized by a severe skin disorder and are useful for identifying compounds and compositions for the treatment of various human diseases.

GENERAL BACKGROUND

The skin as an organ is of interest from biological, medical, and cosmetological points of view. There are a large number of skin diseases that are either organ-specific, e.g. psoriasis and eczemas, or are manifestations of general disease, such as general allergic reactions. The fact that there are skin-specific diseases can be considered as a proof of the existence of molecular mechanisms that are unique for the skin. Analogously, studies on skin-specific molecular processes are of importance for the understanding and treatment of skin disorders. It seems reasonable to assume that several of these processes in one way or another are related to the most specialized function of the skin, that is the formation of a physico-chemical barrier between body exterior and interior. The physico-chemical skin barrier is localized in the outermost layer of the skin, the stratum corneum.

The stratum corneum is the most specialized structure of the skin. It is the end product of the differentiation process of the epidermis, that is the stratified squamous epithelium that accounts for the outermost portion of the skin. The majority of the cells of the epidermis consist of keratinocytes in various states of differentiation. The lowermost keratinocytes,

the basal cells, reside on a basal membrane in contact with the dermis, that is the connective tissue of the skin, and are the only keratinocytes that have dividing capability. A fraction of the basal cells continuously leaves the basal membrane and goes through a differentiation process, which eventually makes the cells become building blocks of the stratum corneum. In this process the keratinocytes go through a number of adaptive changes. There is an increased content of cytoskeleton consisting of epidermis-specific cytokeratins. The intermediate filaments of contiguous cells are joined to a functional unit by an increased number of desmosomes. The most dramatic changes take place during the transition from the uppermost living cell layer, the stratum granulosum, to the non-viable stratum corneum in a process usually called keratinization. Covalently cross-linked proteins are deposited close to the inner aspect of the plasma membrane, forming a very resistant cell envelope. Furthermore a lipid-rich substance, originating in a keratinocyte-specific cell organelle, is secreted to the extracellular space and, by forming lipid lamellae, which surround the cells of the stratum corneum, constitutes the permeability barrier to hydrophilic substances. Finally all intracellular structures except the densely packed cytokeratin filaments disappear.

The cells of the stratum corneum, the corneocytes, are thus non-viable. This means that the regulation of various processes in the stratum corneum must be the result of a "programming" at a state where the keratinocytes are still viable. The turnover of the epidermis, which normally proceeds in about four weeks during which the cells are part of the stratum corneum for about two weeks, is ended by means of cell shedding from the skin surface in the process of desquamation. This process is an example of "programming" of the stratum corneum. A prerequisite for the function of the stratum corneum as a physico-chemical barrier is that its individual cells are held together by mechanically resistant structures, that is desmosomes. The degradation of desmosomes, which is a prerequisite for desquamation, must be regulated so as to give a cell shedding from the skin surface which balances *de novo* production of the stratum corneum without interfering with the barrier functions of the tissue.

Disorders of keratinization

Under a large number of pathological conditions in the skin of varying severity, there are disturbances in the keratinization process. In psoriasis there is, in addition to a typical chronic inflammation, overproduction of an immature stratum corneum resulting in the typical scaling of this disease. There is a group of inherited skin diseases characterized by a thickened stratum corneum which leads to the formation of "fish scales", the so-called ichthyoses. In several of the ichthyoses there is a decreased rate of desquamation. Although less severe than the ichthyoses, "dry skin" (xeroderma) is also characterized by a

stratum corneum from which corneocytes are shed, not as under normal conditions as single cells or as small aggregates of cells, but as large, macroscopically visible scales. This disorder is very common among elderly people and among atopics, that is individuals with a decreased resistance to skin irritants and a disposition to develop a characteristic form of endogenous eczema. In the acne diseases there is a disturbed keratinization in the ducts of the sebaceous glands, which leads to the formation of comedones and plugging. The formation of comedones precedes and is believed to provoke the inflammatory acne lesion.

Proteolytic enzymes are involved in keratinization

There are several stages in the keratinization process and during the turnover of the stratum corneum where proteolytic enzymes seem to play important roles. Certainly the disappearance of all intracellular structures except for the cytokeratin filaments occurring during the transition between viable and cornified epidermal layers must involve proteolysis. The transformation of profilaggrin to filaggrin, a protein that is believed to function in the special type of aggregation of cytokeratin filaments during keratinization, may be catalyzed by a specific proteinase. In the stratum corneum filaggrin is further degraded to low-molecular weight components which are probably important as "natural moisturizers". Furthermore there are proteolytic modifications of cytokeratin polypeptides during the keratinization process. Finally, proteolytic events are likely to play crucial roles in the degradation of intercellular cohesive structures in the stratum corneum in processes eventually leading to desquamation.

Stratum corneum cell cohesion and desquamation. The role of desmosomes

Intercellular cohesion in the stratum corneum as well as in the viable parts of the epidermis is mediated to a significant extent by desmosomes. A desmosome consists of two symmetrical halves, each of which is formed by two contiguous cells. Each desmosomal half has one intracellular part linked to the cytokeratin filaments and one part made up by glycoproteins anchored intracellularly and with transmembranal and extracellular parts. The extracellular parts of these proteins, the desmogleins, are adhesion molecules, and through their interaction with each other in the extracellular space a cohesive structure is formed. The degradation of desmosomes seems to follow somewhat different routes in the stratum corneum of palms and soles as compared to non-palmo-plantar stratum corneum. In the latter tissue around 85% of the desmosomes disappear soon after the cells have become fully cornified. The remaining desmosomes, which are preferentially located at the villous edges of the extremely flattened cells, apparently remain intact up to the level where desquamation takes place. In palmo-plantar stratum corneum the corneocytes are much less flattened, and there is no extensive

degradation of desmosomes in deeper layers of the tissue. In both tissues desquamation is associated with desmosomal degradation. In ichthyotic skin as well as in "dry skin", the number of desmosomes in the superficial layers of the stratum corneum has been shown to be increased.

Many of the tissue-specific molecular mechanisms of the skin are associated with the formation and turnover of the barrier-forming outermost layer of the epidermis, the stratum corneum, consisting of cornified epithelial cells surrounded by highly organized lipids. The stratum corneum is continuously being formed in the process of epidermal differentiation. In the efforts to understand the mechanisms by which a constant thickness of the stratum corneum is maintained via a continuos desquamation of surface cells, two human serine proteases, stratum corneum chymotryptic enzyme (SCCE) and stratum corneum tryptic enzyme (SCTE) have been identified (Hansson et al. 1994 and Brattsand et al. 1999). The cloning and expression of SCCE is described in WO95/00651, which hereby is incorporated by reference. Both enzymes belong to the kallikrein group of serine proteases, the genes of which are localized to a short stretch at chromosome 19q13.3-19q13.4 (Diamandis et al. 2000). SCCE is synonymous with human kallikrein 7 (KLK7). It should be noted however, that the numbering of kallikreins is not consistent between species. The expression of SCCE and SCTE seems to be restricted to squamous epithelia undergoing cornification and in which there is a need for desquamation (Ekholm et al. 2000).

Common inflammatory skin diseases may result in severe handicap by causing reduced function, stigmatization, and almost unbearable sensory symptoms. A dominating symptom of many of these diseases is itch, which in many instances may be extremely troublesome, causing severe disturbances in many aspects of every day life and sleeping patterns of sufferers. In atopic dermatitis, affecting more than 10% of children at some point of their childhood, pruritus is a major diagnostic criterion and always present in active disease. It has even been stated that "atopic dermatitis is an itch that when scratched erupts", and that "pruritus must be considered a quintessential feature of atopic dermatitis" (Beltrani, 1999). The mechanisms of itch are poorly understood, and available treatments are often unsatisfactory. This may be due, at least in part, to lack of satisfactory animal models (Greaves and Wall, 1996).

In inflammatory skin diseases such as psoriasis and atopic dermatitis evidence in favor of a central role for the immune system in pathogenesis is overwhelming. It seems likely that the development of the various disease-specific skin lesions and signs is the result of interactions at the cellular and molecular level between the immune system and skin-derived structures and molecules. In most studies aimed at understanding these

interactions focus has been on cytokines, growth factors, and adhesion molecules. Although many of these components are produced by skin cells, they are not unique for the skin, but are more or less generally present in cells and tissues throughout the body. This fact may cause problems in *e.g.* development of skin-specific therapies. The situation would be different if one could find a truly skin-specific structure or molecule with a central role in the pathophysiology of inflammatory skin diseases. The present invention present new evidence that the serine protease stratum corneum chymotryptic enzyme (SCCE) may belong to this category of skin-specific molecules.

SUMMARY OF THE INVENTION

The present invention relates to results from studies aimed at elucidation of the possible involvement of one of these proteases, SCCE, in skin pathology. The human and murine *scce*-genes were characterized, and transgenic animals overexpressing human *scce* mRNA produced. The only gross phenotypic changes observed in these animals were found in the skin, which showed histological changes with several similarities to those seen in inflammatory skin diseases such as in the chronic stages of atopic dermatitis in humans. In addition, the transgenic animals showed signs of severe itch. Evidence of over-expression of SCCE in chronic lesions of atopic dermatitis in humans was also found corresponding to what has recently been shown in psoriasis (Ekholm et al. 1999). Taken together, the results give support for the idea that SCCE and related enzymes may be involved in the pathophysiology of itchy inflammatory skin diseases, and thus that SCCE may be a potential target for organ-specific treatment strategies. The transgenic animals of the invention may provide a new model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component.

The human SCCE gene was isolated from a human leukocyte genomic library cat. no. HL 1111 j lot # 3511 (Clontech, CA) by using cDNA probes derived from the human *scce* cDNA. Overlapping clones were isolated and the entire structural gene was sequenced by automated DNA sequencing and analyzed by ABI377 (Applied Biosystems, Foster City, CA, USA). The entire sequence can be found using Gene Bank accession no AF 332583.

Table 1 Human SCCE [org=Homo sapiens] Homo sapiens stratum corneum chymotryptic enzyme gene (SEQ ID NO:3).

TACCACATTTTCTTAATCCAGTCTATCACTGATGGACATTTAGGTTGATTCCCTGTGTTTGCTGTTGT
CAATAGTTCTACAATGAACGTACGTGTCCATGTGTCTTTAAACAGAATGATTTATATTCCTTTGGGTA
CACACACTGGGGCTTATGAGAGGGTGGAGAGTGGGAGGAAGGAGAGGATCAGAAAAAAATAACTA

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ATGGGTACTAGGCTTAATACCTGGGTGATTAAATAATCTGTATAACAAACCCCCATGGCGCACGTTC
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AAATATTTGCTTATAAATTAATAAATGAAGCCCTCAAAAATGTTCTATTAGATAATGTTAAGTACAGA
CATTTTTGTTATAAATACATAATATACAAAGAAATCTATGTATAACATGATTAAAATGACCATAAGAA
CATAGATCCTAAACATGGCAAATATTAGTGGGGTGGGGTTAGGGAAAGCGTTGTTTTTAACTTACA
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AGTTCCCCCAGGCGGGCCAGAATTAGGATGTAGGGTCTAGGCCACCCCTGAGAGGGGGTGAGGG
CAAGAAAATGGCCCCAGAAGCCGGGCGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGCGGGGC
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CTGACCGAGGAGCCACTCCAGCCCAGGACACGCCCTCCTACCTGTTCTTCCTGTTTTTCTCCCAGA
ATTC

To isolate the murine *scce* gene cDNA probes derived from the murine *scce* cDNA (Bäkman et al. 1999) were used to screen and isolate clones from a 129SVJ Lambda Fix II genomic library cat. no. 946306 (Stratagene, La Jolla, CA). The entire gene sequence was determined and analyzed as described above. The entire sequence can be found using Gene Bank accession no, AF 339930 which is hereby incorporated by reference and is not shown here.

The amino acid sequences (as deduced from cDNA) of human and murine SCCE show around 80% similarity (Hansson et al. 1994 and Bäckman et al. 1999).

The genomic organization of the human and murine *scce* structural genes are schematically shown in Figure 1. The most apparent difference b tween the structural genes from the two species is that the introns are longer in the human *scce* gene. As seen in Figure 1 the *scce* genes from man and mouse both contain six exons, here indicated as black boxes, and have the translational start located in exon 2, and the stop codon in exon 6. Overall the organization of the exon-intron structures of the two genes is similar but due to shorter introns, the murine gene is smaller, approximately 4kb as compared to 8 kb. In the human gene, the translation initiation site is found 60 nucleotides downstream the 5'-end of exon 2, and a potential TATA-box approximately 35 bp upstream of exon 1. Similarly, the murine initiation codon is positioned within the second exon, 39 nucleotides downstream of the intron-exon junction.

To generate transgenic mice with a modified regulation of expression compared to the endogenous *scce*, recombinant human *scce* gene under control of the *SV40 early* enhancer and promoter element was constructed as described in example 2. Three founders shown to be transgenic for *SV40e-hscce* integrated at a single site were obtained and lines were established by further breeding in C57BL/6JxCBA mice. As expected, initial characterization of the three lines revealed very large differences in levels of recombinant *scce* expression (see below). In line #1010, which has the highest *hscce* transcript levels, skin abnormalities were apparent, whereas in the two other lines no skin changes or other gross phenotypic deviations could be observed. For further detailed comparative studies of the #1010 transgenics one of the lines with apparently normal phenotype (#107) and non-transgenic littermates were included as controls.

The importance of the transcriptional regulation of the recombinant *scce* gene was demonstrated by the results achieved from other variants of transgenic mouse models. In these experiments different regulatory elements were inserted upstream of a genomic fragment comprising the human *scce* structural gene. For example, the mouse/human keratin 14 promoter (Vassar et al.) was utilized with the idea to target the expression of recombinant *scce* to more basal cell layers than is the normal distribution for endogenous SCCE. Also, a long genomic fragment containing the native human *scce* upstream regulatory sequence including the promoter was tested and evaluated. In these experiments the resulting transgenic mice neither showed any signs of altered neither skin morphology nor signs of itch. The detailed construct for recombinant *scce* expression comprising the sv40 early enhancer and promoter elements resulted in a surprisingly restricted distribution of expression and a transgenic mouse having very interesting changes in skin biology and clear signs of itch. This phenotype and expression pattern were surprising since the sv40 early regulatory sequences normally mediates high level

transcription in proliferative cells whereas here the strongest expression in differentiated keratinocytes was observed.

To the knowledge of the present inventors, this is the first report of a mouse model for itchy inflammatory skin diseases produced by genetic manipulation of an enzyme, which may be skin specific. The *SV40-scce* transgenic mice are likely to give new insights into the pathophysiology of itchy human skin diseases and provide a new animal model for development of treatments directed at an organ-specific target. At the RNA-level expression of SCCE can be detected in several organs, although not at levels comparable to skin (Hansson et al. 1994 and Brattsand et al. 1999). In non-malignant tissues SCCE protein has so far been found only in high suprabasal cells in squamous epithelia undergoing cornification and with a need for desquamation (Ekholm et al. 2000 and Ekholm et al 1998). The present inventors show here that over-expression of SCCE in mice at a site close to where it is normally expressed leads to a condition which to some extent simulates common, often debilitating human skin diseases such as atopic dermatitis and psoriasis.

In SV40-*scce* transgenic mice with phenotypic skin changes expression of transgenic SCCE, RNA as well as protein, was found also in other organs, especially small and large intestine, and lungs. The fact that no pathological changes were seen in these organs may be explained either by a resistance or unresponsiveness to effects mediated by SCCE, or by a lack of SCCE-activating enzymes in unaffected organs. SCCE, human as well as murine, is produced as an inactive precursor, which is converted to active protease by tryptic cleavage at a conserved site (Hansson et al. 1994 and Bäckmann et al. 1999). The enzyme responsible for SCCE-activation in the epidermis has not yet been identified.

The *SV40-scce* transgenic mice had a somewhat unexpected expression pattern of SCCE in the skin. Since the transgene construct contained the *SV40* promoter it was expected to find the highest expression at sites with proliferating keratinocytes, i.e. in the basal layer of the epidermis and in hair follicles. On the contrary, no evidence of SCCE-expression was found in basal cells. Instead, as found by immunohistochemistry, there was expression in suprabasal cells, the intensity of which continuously increased with distance from the basal layer. This pattern is similar to that seen in psoriasis (Ekholm et al. 1999) lesions and chronic lesions in atopic dermatitis in humans. A possible explanation may be that the human *scce*-gene contains internal regulatory elements that suppress its expression in undifferentiated keratinocytes in the epidermis.

The mechanisms by which SCCE can cause a thickened epidermis with hyperk ratosis, a dermal inflammatory infiltrate, and itch remain to be elucidated. According to the current

view the SCCE precursor is synthesized in high suprabasal epidermal keratinocytes and stored in lipid rich lamellar bodies. In the process in which a terminally differentiated keratinocyte is transformed from a viable cell to a corneocyte, i. e. a building block of the cornified surface layer of the epidermis - the stratum corneum - the contents of the lamellar bodies, including SCCE-precursor, are secreted to the extracellular space, where conversion of pro-SCCE to active protease is taking place (Sondell et al. 1995). One possibility is that SCCE, which has been activated as postulated, diffuses through the epidermis to the superficial parts of the dermis, thereby inducing epidermal thickening as well as dermal inflammation and activation of itch-mediating nerve endings. In previous studies on proteases as potential mediators of itch the enzymes were injected intradermally in human volunteers. Injection of trypsin and mast cell chymase caused itch by a mechanism believed to involve release by mast cells of histamine, whereas the itch caused by intradermally injected kallikrein appeared to be mediated by a mechanism not involving histamine (Hägermark et al. 1972 and Hägermark (1974). Treatment with an antihistaminic drug appeared not to relieve the itch seen in *SV40-scce* transgenic mice (A. Ny and T.Egelrud, unpublished observation). The fact that SCCE detected by immunohistochemistry in skin of SV40-*scce* transgenic mice was confined to superficial parts of the epidermis suggests that the dermal inflammation and the pruritus observed in these mice were not direct effects of active SCCE. In addition, signs of itch were not seen before the age of around 5 weeks, whereas overexpression of SCCE was found also in younger animals. An alternative explanation to the changes and signs caused by over-expression of SCCE in the epidermis could be that an increased proteolytic activity in the transition zone between viable epidermal layers and the stratum corneum may lead to release of mediators, which diffuse to other parts of the skin where they cause epidermal changes, dermal inflammation, and pruritus. A third possibility is that the epidermal hyperkeratosis and achantosis, dermal inflammation and pruritus are results of adaptive responses to a deterioration of the barrier function of the stratum corneum caused by increased proteolytic degradation of structures responsible for intercellular cell cohesion in the cornified layer. The proliferative response of the epidermis could be a result either of a direct effects of the released mediators on keratinocytes or an effect which is secondary to the dermal inflammation.

Recently a direct association between a defective epidermal barrier function and aberrant proteolysis in an inherited human condition with severe skin disease was described. Strong evidence was presented that the disease-causing mutations in Netherton's syndrome are localized to a gene coding for a precursor of serine protease inhibitors (Chavanas et al. 2000). These results, together with the present results, suggest that increased activity of serine proteases in the skin may indeed play a significant role in skin pathophysiology.

They also provide incentives for further exploring of possible new therapeutic principles for skin diseases.

DETAILED DISCLOSURE OF THE INVENTION

The present invention relates to a non human transgenic mammal or mammalian embryo having integrated within its genome a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of the heterologous *scce* or a variant thereof in skin.

By the term "heterologous" is referred to a DNA sequence inserted within or connected to another DNA sequence which codes for polypeptides not coded for in nature by the DNA sequence to which it is joined. Allelic variations or naturally occurring mutational events do not give rise to a heterologous DNA sequence as defined herein.

Preferably, the present invention relates to a transgenic mammal or mammalian embryo having integrated within its genome a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of *scce* in epidermis.

By the term "a human stratum corneum chymotryptic enzyme (SCCE)" is meant a serine protease having the amino acid sequence SEQ ID NO:2 described in WO95/00651 and shown in the enclosed sequence listing. SCCE is synonymous with human kallikrein 7 (KLK7). However, the numbering of kallikreins is not consistent between species. As discussed in example 6 the rat KLK7 in (Kroon et al. 1977) does not seem to be the rat SCCE. By the term "a SCCE variant" is meant a variant of said sequence not having exactly the amino acid sequence shown in SEQ ID NO:2, it may e.g. be a SCCE protease from another species, such as from a cow, pig, rat or mouse, or a synthetic polypeptide comprising a part of SEQ ID NO:2. The SCCE variant will generally react with antibodies raised against purified native or recombinant human SCCE and will generally have significant "SCCE activity", i.e. be a serine proteinase which can be inhibited by the same inhibitors as the spontaneous cell dissociation that can be induced in model systems with samples of cornified layer of skin incubated at neutral or near neutral pH at physiological temperature, i.e. about 37°C, as described in WO95/00651.

As can be seen from the following tables, there are significant similarities between SCCE from different species:

Table 2. Alignment of partial deduced amino acid sequences from different species, corresponding to residues 162-184 of human SCCE (Hansson et al.1994). In bold are shown the residues Asn-170 and Ser-176.

Cow SCCE	NH2...AGIPNSRT**N**ACNGD**S**GGPLMCKG...	(SEQ ID NO:4)
Pig SCCE	NH2...AGIPNSKT**N**ACNGD**S**GGPLVCKG...	(SEQ ID NO:5)
Hum SCCE	NH2...AGIPDSKK**N**ACNGD**S**GGPLVCRG...	(SEQ ID NO:6)
Rat SCCE	NH2...AGIPDSKT**N**TCNGD**S**GGPLVCND...	(SEQ ID NO:7)
Mouse SCCE	NH2 AGIPDSKT**N**TCNGD**S**GGPLVCND...	(SEQ ID NO:8)

The bottom of the primary substrate specificity pouch (see Hansson et al., 1994) in SCCE from different species (residue no 170 in Table 2 above) contains a conserved asparagine residue, which is unique among known serine proteases. Also the sequence between this residue and the active serine residue (no. 176 in Table 2) is highly conserved. This suggests that the function, e.g. specialized catalytic properties, of SCCE is critically dependent on the mentioned asparagine residue.

Table 3 Alignment of partial deduced amino acid sequences from different species, corresponding to residues (-)7 - 27 of human SCCE (Hansson et al.1994). In bold are shown the residues adjacent to activation site (C-terminal of Lys-(-1) of Arg (-1).

Cow SCCE ..	QEDQGNKS**GEKIID**GVPCPRGSQPWQVALLKGSQLHCG...	(SEQ ID NO:9)
Pig SCCE ..	QEGQDKS**GEKIID**GVPCPGGSRPWQVALLKGNQLHCG...	(SEQ ID NO:10)
Hum SCCE	....EEAQ**GDKIID**GAPCARGSHPWQVALLSGNQLHCG...	(SEQ ID NO:11)
Rat SCCE	....Q**GERIID**GYKCKEGSHPWQVALLKGDQLHCG...	(SEQ ID NO:12)
Mouse SCCE	....Q**GERIID**GIKCKEGSHPWQVALLKGNQLHCG...	(SEQ ID NO:13)

Active human SCCE is formed by cleavage C-terminal of K in the sequence KIIDG etc. This activation can be catalyzed by trypsin in vitro (Hansson et al., 1994).
Examining the amino acid sequence adjacent to this cleavage site reveals a high degree of conservation between species. The consensus sequence is G-X_1-X_2-I-I-D-G (SEQ ID NO:14), where X_1 is either aspartate (D) or glutamate (E), and X_2 is either lysine (K) or arginine (R). Aspartate and glutamate are functionally similar, both having negatively charged functional groups. The same holds true for lysine and arginine, which both have positively charged functional groups and forms sites for cleavage catalyzed by enzymes with trypsin-like primary substrate specificity. The consensus sequence adjacent to the

activation site is unique among known serine proteases, suggesting an important function. It also suggests that there may exist enzymes in tissue (e.g.) epidermis, the specific function of which is SCCE-activation.

More specifically, the invention relates to a transgenic mammal or mammalian embryo having integrated within its genome a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a protein with an amino acid sequence which has a sequence identity of at least 75% to the amino acid sequence shown in SEQ ID NO:2 and which contains the partial sequence glycine-X_1-X_2- isoleucine-isoleucine-aspartate-glycine (SEQ ID NO:14), wherein X_1 is aspartate or glutamate and X_2 is lysine or argininine, operably linked to a promoter that drives expression in skin.

Preferably, the invention relates to a transgenic mammal or mammalian embryo having integrated within its genome a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a protein with an amino acid sequence which has a sequence identity of at least 75% to the amino acid sequence shown in SEQ ID NO:2 and which contains the partial sequence (SEQ ID NO:15) X_3-asparagine-X_4-X_5-X_6 X_7-X_8-serine, wherein
X_3 is any amino acid residue, X_4 is any amino acid residue, X_5 is a cystein residue X_6 is any amino acid., X_7 is a glycine residue, X_8 is an aspartate residue, and the serine is the active serine residue characteristic of serine proteases, operably linked to a promoter that drives expression in skin.

In alternative embodiments, the encoded polypeptide has a sequence identity of at least 80% with the amino acid sequence shown in SEQ ID NO:2, such as at least 90%, e.g. at least 95%, preferably at least 98%, e.g. at least 99%.

To determine the percent identity of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., % identity= # of identical positions/total # of positions (e.g., overlapping positions) x 100). In one embodiment the two sequences are the same length.

Alignment of two sequences for the determination of percent identity can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecule of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing the NBLAST, XBLAST, and Gapped BLAST programs, the default parameters of the respective programs can be used. See http://www.ncbi.nlm.nih.gov. Alternatively, sequence identity can be calculated after the sequences have been aligned e.g. by the program of Pearson W.R and D.J. Lipman (Proc Natl Acad Sci USA 85:2444-2448, 1998) in the EMBL database (www.ncbi.nlm.gov/cgi-bin/BLAST). Generally, the default settings with respect to e.g. "scoring matrix" and "gap penalty" can be used for alignment.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

By the term "at least a significant part of a nucleotide sequence coding for SCCE" is meant a nucleotide sequence (i.e. a DNA sequence or a RNA sequence) encoding a polypeptide having at least a part of the amino acid sequence shown in SEQ ID NO:2 and preferably resulting in an abnormal phenotype as described in the following. It is contemplated that it is useful and maybe even necessary to include intron sequences when preparing a nucleotide sequence coding for a SCCE or a variant thereof, i.e. one or more of the introns present in the human *scce* shown in Table 1 (see also annotations to GenBank accession number AF332583 which hereby is incorporated by reference) or one or more of the murine introns which may be deduced from the murine sequence. It is likely that not all of the intron sequences are necessary and that intron sequences from SCCE from other species or intron sequence from genes coding for other proteins may also be suitable and should be inserted in the nucleotide sequence coding for SCCE in a suitable manner.

It is contemplated that only a minor part of SCCE is necessary in order to obtain the abnormal phenotype. By the term "a significant part" is meant a nucleotide sequence encoding at least 50 amino acids of SEQ ID NO:2, e.g. at least 70 amino acids, at least 100 amino acids, at least 150 amino acids or at least 200 amino acids. These lengths are considered to be "a significant part of the peptide shown in SEQ ID NO:2". The polypeptides encoded may be longer than the above stated lengths, which will then indicate the parts which are common between the polypeptides encoded and SEQ ID NO:2. Generally, however, such nucleotide sequences will comprise the major part of the nucleotide sequence shown in SEQ ID NO:1 described in WO95/00651 and shown in the enclosed sequence listing, such as at least 500 nucleotides, e.g. at least 600 nucleotides, at least 650 nucleotides, at least 700 nucleotides, e.g. 750 nucleotides.

Such nucleotide sequences will generally hybridize with the complementary sequence to nucleotide sequence SEQ ID NO: 1 or a part thereof under stringent hybridization conditions. Within the concept of the present invention is thus a transgenic mammal or mammalian embryo having integrated within its genome a nucleotide sequence which hybridizes with the complementary sequence to the nucleotide sequence SEQ ID NO: 1 or a part thereof under stringent hybridization conditions, preferably under highly stringent conditions, said sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of *scce* in skin. In a particularly interesting embodiment of said transgenic mammal or mammalian embryo said promoter drives expression of *scce* in epidermis. The term "stringent" when used in conjunction with hybridization conditions is as defined in the art, i.e. 15-20°C under the melting point T_m, cf. Sambrook et al, 1989, pages 11.45-11.49. Preferably, the conditions are "highly stringent", i.e. 5-10°C under the melting point T_m. However, due to the degeneracy of the genetic code also nucleotide sequences, which have only minor resemblance to SEQ ID NO:1, may be able to encode a SCCE.

The vectors for expressing the nucleic acids having nucleotide sequences coding for a SCCE require that the nucleic acid having a nucleotide sequence coding for a human SCCE be "operatively linked." A nucleic acid is operatively linked when it is placed into a functional relationship with another nucleic acid sequence. For instance, a promoter or enhancer is operatively linked to a coding sequence if it affects the transcription of the sequences. The promoter and enhancer may be the same or two different entities. The SV40 early promoter is an example of an integrated promoter and enhancer. Operatively linked means that the DNA sequences being linked are contiguous and, where necessary to join two protein-coding regions, contiguous and in reading-frame. By the term "a SCCE construct" is meant a nucleotide sequence comprising at least a significant part of a

nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of *scce* in skin or part of the skin. In particular a SCCE construct that comprise a promoter that drives expression of *scce* in epidermis is contemplated.

In a preferred embodiment according to the present invention, the promoter is a ubiquitous promoter. By the term "ubiquitous promoter" is meant a promoter that is active in many different cell types of the host organism in contrast to a promoter whose expression is specific for one or a few target cell types (a tissue-specific promoter). An example of "ubiquitous" promoter" is the SV40 promoter and variations thereof such as the SV40 early promoter. Other examples of ubiquitous promoters are other viral promoters such as polyoma early promoter, retroviral long terminal repeats (5'-LTR) adenovirus promoters, and house keeping cellular genes such as β-actin, and ribosomal protein promotors. The promoter is preferably a heterologous promoter. It is contemplated that constitutive viral promoters, such as polyoma early viral promoter, Ebstein Barr virus promoter and retroviral long term repeat LTR promoters will be useful in the construction of transgenic mammals according to the invention.

An important embodiment of the invention relates to a transgenic mammal or mammalian embryo selected from the group consisting of rodents, such as mice, rats and rabbits, cats and dogs. A preferred embodiment of the invention is a transgenic mammal or mammalian embryo, which is selected from the group consisting of mice.

Preferably, the transgenic mammal or mammalian embryo according to the invention comprises a heterologous nucleotide sequence comprising a significant part of DNA sequence coding for human SCCE as shown in SEQ ID NO:1. The transgenic mammal or mammalian embryo according to the invention preferably comprises a nucleotide sequence coding for a significant part of the peptide shown in SEQ ID NO. 2 as defined above. In preferred embodiments, the DNA sequence codes for the peptide corresponding to amino acid no. -7 through no. 224 of the amino acid sequence shown in SEQ ID NO. 2, the peptide corresponding to amino acid no. 1 through no. 224 of the amino acid sequence shown in SEQ ID NO. 2 or the peptide shown in SEQ ID NO. 2. Presently preferred embodiments relate to transgenic mammals or mammalian embryos according to the invention, wherein the DNA sequence comprises the DNA shown in SEQ ID NO. 1 or the DNA sequence is SEQ ID NO:1.

In an important embodiment of the invention, the transgenic mammal or mammalian embryo according to the invention exhibits an abnormal phenotype, such as an abnormal skin phenotype and/or a predisposition for cancer, e.g. a predisposition for ovarian cancer.

Preferably, the mammal or mammalian embryo according to the invention exhibits an abnormal skin phenotype resembling one or more inflammatory skin diseases characterized by epidermal hyperkeratosis, acanthosis, epidermal and/or dermal inflammation and/or pruritus, e.g. inherited skin diseases with epidermal hyperkeratos, ichthyosis vulgaris, psoriasis, chronic atopic dermatitis or chronic eczema. The mammal or mammalian embryo according to the invention may thus exhibit epidermal hyperkeratosis, achantosis, epidermal/dermal inflammation and/or pruritus.

The invention further relates to a method for making a transgenic non human mammal or mammalian embryo having integrated within its genome a heterologous nucleotide construct comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of *scce* or a variant thereof in skin, the method comprising

(a) constructing and amplifying a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or a variant thereof operably linked to a promoter that drives expression of *scce or a variant thereof* in skin,

(b) introducing into a non-human cell said heterologous nucleotide construct,

(c) using said cell or the progeny of said cell to create a number of putative transgenic non-human mammals or mammalian embryos,

(d) selecting said non-human mammal or mammalian embryo having said heterologous nucleotide construct integrated within its genome.

In one embodiment of the invention said transgenic mammal or mammalian embryo have integrated a nucleotide sequence coding for human SCCE or a variant thereof as defined above operably linked to a promoter that drives expression of *scce* in epidermis. In a preferred embodiment, the invention relates to a method for making a transgenic mammal according to the invention, where the mammal exhibits an abnormal phenotype as defined above. The method comprises introducing the SCCE-construct into an ovum or embryo of the mammal by physical, chemical or viral means, e.g. by electroporation, transfection, microinjection or viral infection. In a preferred embodiment of the invention, the SCCE-construct is microinjected into an ovum or embryo of the mammal or into embryonal stem cells of the mammal. In a preferred embodiment, the method according to the invention comprises microinjecting the SCCE-construct into C57BL/6JxCBA-f2 mice ovum or embryos. The method preferably further comprises breeding the resulting mice with

C57BL/6JxCBA or with C57BL/6J to btain transgenic litter and stable mouse lines. Such stable cell lines derived from the transgenic mammals comprising a SCCE construct as described above are contemplated to be useful for e.g. high throughput screening of suitable compounds as described in the following.

Another aspect of the invention relates to the use of the transgenic mammal or mammalian embryo according to the invention as a model for the study of disease with the aim of improving treatment, relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation or for the development of a diagnostic method. A preferred use according to the invention of said transgenic mammal or mammalian embryo is as a model for a skin disease or a model for cancer such as ovarian cancer.

An important aspect of the invention relates to a method of screening for a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, the method comprising

(a) administering a compound or composition to a transgenic mammal having integrated within its genome a nucleotide sequence coding for at least a significant part of SCCE operably linked to a promoter that drives expression of the *scce* in an organ, wherein the rodent exhibits an abnormal phenotype,

(b) evaluating the appearance of the relevant organ and/or the behavior of a mammal treated according to step (a), and

(c) comparing the appearance of the relevant organ and/or the behavior of a treated rodent with an untreated control mammal.

An important aspect of the invention relates to a method of identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, the method comprising

(a) administering a compound or composition to a transgenic mammal having integrated within its genome a nucleotide sequence coding for at least a significant part of SCCE operably linked to a promoter that drives expression of the *scce* in an organ, wherein the rodent exhibits an abnormal phenotype,

(b) evaluating the appearance of the relevant organ and/or the behavior of a mammal treated according to step (a), and

(c) comparing the appearance of the relevant organ and/or the behavior of a treated rodent with an untreated control mammal.

(d) identifying the compound or composition as being effective for the prevention or treatment of the abnormal or unwanted phenotype.

In preferred embodiments, the organ is the ovaries or the skin, or more preferably the epidermis. A presently preferred embodiment of the invention relates to a method of screening for or identifying a compound or composition effective for the prevention or treatment of itchy inflammatory skin diseases such as ichthyosis vulgaris, prurigo nodularis, neurodermatitis, lichen planus. Other preferred embodiments of the invention relate to a method of screening for or identifying a compound or composition effective for the prevention or treatment of chronic atopic dermatitis and psoriasis. Also, the invention relates to a method according to the invention for screening of a cosmetic composition.

Another important aspect of the invention relates to a method of preparing a pharmaceutical composition which comprises: i) identifying a compound or composition as being effective for the prevention or treatment of an abnormal or unwanted phenotype using a method according the present invention, and ii) mixing the compound with a pharmaceutically acceptable excipient or diluent.

In particular, the invention relates to a cosmetic or pharmaceutical composition that has been discovered or developed by use of the above methods comprising use of a transgenic mammal or mammalian embryo as described above. In this respect the invention relates to pharmaceutical formulations for systemic treatment as well as for cosmetic and pharmaceutical formulations for topical application on the skin or epithelium.

Yet a further aspect of the invention relates to a method of treating or preventing an abnormal or unwanted phenotype which method comprises administering to a patient suffering from such an abnormal or unwanted phenotype a pharmaceutical composition prepared according to a method of the present invention.

A preferred embodiment of the invention relates to a method of treating or preventing itchy inflammatory skin diseases such as ichthyosis vulgaris, prurigo nodularis, neurodermatitis, lichen planus. Other preferred embodiments of the invention relate to methods of treating or preventing chronic atopic dermatitis and psoriasis.

LEGEND TO FIGURES

Figure 1.

Organization of the human and murine structural genes and the recombinant *sv40e/hscce* gene. The six exons are indicated as black boxes. The translational start sites, located in exon 2, are indicated with "ATG", and the stop codons in exon 6 with "TAA". Also the position of the *sv40e* transcriptional regulatory element in the construct used to generate the transgenic animal is indicated by an arrow.

Figure 2

pS99.

Figure 3.

A: Real time quantitative PCR analyses of recombinant human *scce* mRNA in various tissue preparations from the transgenic lines #1010 (*black bars*) and #107 (*empty bars*). Analyses in triplicate were carried out on RNA samples comprising pooled material from three animals from each line. The murine acidic ribosomal phosphoprotein P0 was used as internal standard. Mean and SD.

B. ELISA-analyses of SCCE-protein in various tissues from the transgenic lines #1010 (*black bars*) and #107 (*empty bars*), and non-transgenic siblings (*gray bars*). Analyses in triplicate were carried out on pooled extracts from three animals from each line and controls. Mean and SD.

Figure 4

Pro-SCCE and active SCCE in skin from #1010 *scce*-transgenic mice. *Hu* = extract of human plantar stratum corneum; *Tg* = extract of skin from #1010 transgene; *Wt* = extract of skin from wild type littermate. Approximately 0.1 g of mouse skin was homogenized in 10 ml of 1 M acetic acid and extracted over night at 4 °C. After clearing by centrifugation extracts were aliquoted, lyophilized, and resolubilized in electrophoresis sample buffer.

A: Immunoblot with SCCE-specific antibodies, reduced samples. Arrowheads denote, from top to bottom, glycosylated pro-SCCE, mixture of unglycosylated pro-SCCE and glycosylated SCCE, and unglycosylated SCCE. Amount of sample applied corresponding to 0.1 mg and 4.5 mg of skin for Tg and Wt, respectively.

SUB B5

B: Zymography in 12.5% acryalmide gel with 1% casein; non-reduced samples. Amount of sample applied corresponding to 0.4 mg and 4.5 mg of skin for Tg and Wt, respectively. Arrow denotes SCCE.

To the far left (marked by asterisks) molecular weight markers; from top 106, 81, 47.5, 35.3, 28.2, and 20.8 kDa respectively

Figure 5.

Scratching behavior of *scce*-transgenic (#1010) mice. Twenty one mice, (11 transgenes, 5 females; 10 wild type litter mates, 2 females) were observed every fifth day for 45 days, starting when the mice were 5-6 weeks of age. At each observation point mice were transferred to individual cages, and episodes of scratching with hind or front paws were counted during three 5-min periods with 2.5 min lapsing from the transfer to the cage to the first counting, and between counting periods. The results for the three observation periods were pooled and the number of episodes of scratching per min calculated. In A the number of episodes of scratching (mean and SEM for all animals in each group) is shown, in B the percentage of animals with at least one episode of scratching per min is given. ■ (square) = #1010 transgenic mice; ▲ (triangle) = wild type litter mates.

Figure 6.

Histology and SCCE-immunohistology of skin from *scce* #1010 transgenic mouse and control; comparison with normal human skin and chronic lesion of atopic dermatitis. Formaldehyde fixed and paraffin embedded samples. A-B stained with hematoxylin and eosin. C-F immunoperoxidase staining with SCCE-specific antibodies, contra-staining with hematoxylin. A and C: #1010 transgenic mice, 5 weeks of age. B and D: non-transgenic littermate. E: Atopic dermatitis. F: Normal human skin. *Bar* = 50 μm.

Figure 7.

The effect on itch in *scce*-transgenic mice of the glucocorticoid triamcinolone acetonide. Squares = triamcinolone acetonide, n = 4; triangles = controls (saline), n = 6. * = statistically significant difference ($p < 0.05$) between controls and treated group.

Figure 8.

The effect on itch in scce-transgenic mice of the antihistamine loratidine. Black bars = loratidine (n = 7); White bars = controls (n = 7); mean and SE.. There were no statistically significant differences in frequency of scratching between treatment group and control group.

EXAMPLES

The following examples are provided for illustration and are not intended to limit the invention to the specific examples provided.

EXAMPLE 1.

Isolation and cloning of the human SCCE gene.

The human SCCE gene was isolated from a human leukocyte genomic library cat. no. HL 1111 j lot # 3511 (Clontech, CA) by using cDNA probes derived from the human *scce* cDNA. A 253 bp cDNA fragment was amplified from pS500 (Hansson et al., 1994) by PCR using SYM3300 (5'-GGTGGCCCTGCTCAGTGGCA-3') (SEQ ID NO: 16) and SYM3301 (5'-CACCATGGATGACACAGCCTGG-3') (SEQ ID NO: 17), ^{32}P-labelled by random priming using oligo-labelling kit (Amersham, UK) and used as a probe for screening. The fragment covers bases 149 to 401 of the published human SCCE cDNA sequence (Hansson et al., 1994). Approximately 5x10^5 plaques were screened. Filters were prepared, prehybridized and hybridized at 65 °C, and washed at 65 °C and 25°C in accordance with the membrane manufacturers recommendations (Colony/Plaque Screen™ hybridization transfer membranes DuPont NEN, MA). Filters were exposed to Hyperfilm-MP (Amersham, UK). After three rounds of screening, individual positive clones were selected, and phage DNA was isolated using standard techniques (Sambrook et al., 1989). Phage DNA was digested with several restriction enzymes and Southern blotting was performed using three different probes. First, the 253 bp 5'-fragment described above was used. Second, a 618 bp 3'-noncoding cDNA fragment was used as a probe. The fragment was amplified by PCR using pS501 as template, forward primer SYM3302 (5'-AATAAAGAAACACAAAACCC-3') (SEQ ID NO: 18) and reverse primer SYM3418 (5'-TGTAATATCATTGTGGGC-3') (SEQ ID NO: 19). pS501 is a plasmid containing 1888bp human SCCE cDNA isolated from a λgt11 keratinocyte cDNA library ligated into EcoRI site of pUC19 and covers cDNA with coding sequence from amino acid four over the stop codon and contains 868 bp extra untranslated 3' sequence. Finally, a 897 bp fragment containing the entire coding SCCE cDNA sequence was isolated from EcoRI/DraI digested pS500 (Hansson et al., 1994) and used as a probe. Probes were labelled and hybridization was performed as described above. Two positive clones were digested with SalI and cloned into pUC19 generating pS772 and pS773. In order to determine the DNA sequence of the human SCCE gene, several overlapping subclones of pS772 and pS773 were generated in pUC19. Subclones were sequenced using the dideoxy chain termination method (T7 sequencing kit, Pharmacia, Sweden or the Dye Terminator Cycle Sequencing Ready Reaction kit, PE Applied Biosystems, CA) with M13 forward and reverse primers as well as specific primers..

Isolation and cloning of the mouse SCCE gene.

To isolate the murine SCCE gene, a 430 bp cDNA fragment was isolated from HindIII/SalI digested pS506 (Bäckman et al., 1999). The fragment was ^{32}P-labelled by random priming using oligo-labelling kit (Amersham, UK), and used as probe to screen a 129SVJ Lambda Fix II genomic library (Stratagen, CA). Approximately 1x10^6 plaques were screened. The blots were prepared, prehybridized and hybridized at 65 °C as described by the manufacturer (Colony/Plaque Screen™ hybridization transfer membranes DuPont NEN, MA). Washing was also performed as described in the hybridization protocol and membranes were exposed to Hyperfilm-MP (Amersham, UK). Individual positive clones were selected after three rounds of screening. A few positive plaques were further investigated by PCR using SYM4118 (5'-GGATGTGAAGCTCATCTC-3') (SEQ ID NO: 20) and SYM4121 (5'-TGGAGTCGGGGATGCCAG-3') (SEQ ID NO: 21). Obtained PCR products were analyzed by Southern blotting using the probe and conditions described above. Phage DNA was isolated from confirmed positive clones using standard techniques. Southern analysis was performed on phage DNA digested with a panel of restriction enzymes using the probe and conditions described above. One of the positive clone was digested with SacI, and a fragment of ~15.5 kb was isolated and cloned into pUC19 generating pS714. Several overlapping subclones of pS714 were generated in pUC19. DNA sequencing of the subclones were performed as described for the human SCCE gene.

Primer extension analysis.

Two exon 1-specific oligonucleotides; one human and one mouse, were used to determine the 5'-prime ends of the human and murine SCCE transcripts. To determine the start of the human transcript (Ausubel et al.) a PCR fragment of 346 bp was amplified from plasmid pS779 (A subclone covering 5'-untranslated sequence, exons 1-3, 5'-end of exon 4 and introns 1-3) using forward primer SYM4720 (5'-GGGAGGGTGGAGAGAGA GTGCAGTG) (SEQ ID NO: 22) and reversed primer SYM4899(5'-AGTCTAGGCTGCAG CCCCTAC-3') (SEQ ID NO: 23). To prepare a 245 bp ^{32}P-dCTP labelled single stranded probe, primer hEXON1 (5'-CTCGAGGGATCTGATGTGATCC-3') (SEQ ID NO: 24) was annealed to the amplified fragment and labelling was performed using the Prime-A-Probe TM DNA labelling kit (Ambion, Austin, Texas, USA). 10^6 cpm labelled probe was mixed with 50 µg total RNA from human skin. Hybridisation and S1 treatment was performed using S1-Assay™ (Ambion, Austin, Texas, USA). The final product was analyzed on a sequencing gel. Dideoxy sequencing reactions of pS779 primed with oligo hEXON1 were used as size markers.

The start of the murine transcript was determined using SacI linearized pS721 (A subclone covering 5'-untranslated sequence, exons 1-3, introns 1-2 and 5'-end of intron 3). A 225 bp ^{32}P-dCTP labelled single stranded probe was prepared by annealing of primer mEXON1

(5'-CTGGGAGTGACTTGGCGTGGCTCT-3') (SEQ ID NO: 25) to the linear plasmid and labelling was performed using the Prime-A-Probe TM DNA labelling kit (Ambion, Austin, Texas, USA). 10^6 cpm labelled probe was mixed with 50 µg total RNA isolated from mouse tail. Hybridization and S1 treatment was performed using S1-Assay™ (Ambion, Austin, Texas, USA). The obtained product was analyzed as described above using sequencing reactions of pS721 primed with oligo mEXON1 as size markers.

RESULTS

(Nucleotide sequences in Gene Bank: Human *scce* (hSCCE): accession number AF332583; Murine *scce* (mSCCE): Acession number AF339930.)

A human leukocyte EMBL3λ genomic library was screened using a probe made from the coding region of human *ssce* cDNA (Hansson et al., 1994) individual positive clones were identified. Based on restriction analysis and Southern blotting two overlapping clones, 12 and 15.5 kbp in size respectively, were selected. These clones were spanning the entire *scce* cDNA. The genomic structure of the human *scce* structural gene comprises six exons and spans approximately 8 kb. The organization and sizes of exons and introns are shown in fig 1. The translation initiation site (designated +1) is found 60 nucleotides downstream the 5'-end of exon 2.

To isolate the murine *scce* gene, a SVJ129 genomic λFIX™ II library was screened using a probe corresponding to the coding region of murine *scce* cDNA (Bäckman et al.). Among the isolated clones one harboring about 15.5 kb was shown to contain the entire murine structural gene. A major part comprising 11770 nucleotides was sequenced and the murine structural *scce* gene was shown to be shorter than the human gene. However, the overall organization reveals several similarities with the human homologue and also consists of six exons (figure 1). Since the polyadenylation site of the murine cDNA has not been identified so far, the exact size of exon 6 could not be determined. However, a putative poly A site was localized 136 bp 3'-prime of the stop codon. The translation initiation site (designated +1) is found in exon 2, 39 nucleotides 3' of the intron 1 3'-intron-exon junction.

To determine the 5' ends of the human and murine transcripts primer extension studies were performed. Sequence analysis of the human cDNA (exon1, unpublished results) revealed that the major human primer extension product extends to the nucleotide identified at the 5' end of the human cDNA sequence (Hansson et al). Analysis of the two major products obtained from the murine gene by primer extension reveal two different transcription starts. One product extends to one nucleotide 5' of the murine SCCE cDNA 5' end (Bäckman et al.). The other product extends to one nucleotide 3' of the cDNA 5' end.

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EXAMPLE 2

Generation and gross phenotypic characterization of of scce transgenic mice with the hscce gene under control of the SV40e promoter

Construction of transgene.

In order to overexpress the human genomic *scce* structural gene under transcriptional regulation of the simian virus 40 early, *SV40e,* enhancer and promoter, an expression vector was constructed. The *scce* genomic DNA was modified by insertion of *Hind*III linkers 20 bp upstream of the start codon and 4.8 kb downstream of the stop codon, respectively. The resulting *Hind*III *scce* fragment was the ligated to a 325 bp *Bam*HI/*Hind*III fragment of pS99 (Figure 2) containing the *SV40e* enhancer and promoter elements and cloned into pBluescript SK+/- (Stratagene) resulting in pAM119. For gene transfer, the plasmid pAM119 was digested with *Bam*HI and *Cla*I and the *SV40e/scce* fragment of about 10.7 kb was isolated and purified by electroelution before microinjection into one-cell stage mouse ova.

Transgenic mice were generated in C57BL/6JxCBA-f2 embryos by standard microinjection procedures (Hogan et al, 1986). The 10,7 kb SV40e/scce fragment to be injected was excised from the pAM119 plasmid by restriction enzyme cleavage with BamHI and ClaI, separated by gel electrophoresis through an agarose gel, cut out, isolated using isotachophresis and precipitated with ethanol.

Identifying transgenic animals.

To identify transgenic animals, DNA was extracted from tail biopsies of 3-wk old mice and the DNA was analyzed either by Southern blot analyses or with PCR as described in Ausubel et al. The PCR analysis was performed using primers specific for human *scce* (IE2: 5´-GCT CTC CCA TTA GTC CCC AGA GA-3´ (SEQ ID NO: 26) ,MJ2: 5´-CCA CTT GGT GAA CTT GCA CAC TTG-3´ (SEQ ID NO: 27)). Briefly, the PCR was performed with an initial denaturation at 95 °C for 10 min., followed by 28 cycles of denaturation at 95 °C for 30 sec, annealing at 65 °C for 30 sec, elongation at 72 °C for 45 sec and finally by a 10 min elongation at 72 °C. The resulting PCR products were analyzed by standard agarose gel electrophoresis using a 1 % agarose gel and visualizing the DNA with Ethidium bromide as described in Ausubel et al., 1992. Three transgenic lines (#103, #107 and #1010) were established by breeding heterozygous mice with C57BL/6JxCBA.

RESULTS

As expected, initial characterization of the three lines revealed very large differences in levels of recombinant *scce* expression (see example 3). In line #1010, which has the highest *hscce* transcript levels, skin abnormalities were apparent, whereas in the two other lines no skin changes or other gross phenotypic deviations could be observed. For further detailed comparative studies of the #1010 transgenics one of the lines with apparently normal phenotype (#107) and non-transgenic littermates were included as controls. Macroscopic phenotypic changes in transgenic #1010 animals were noted as a loss of hair from a narrow zone around the eyes in mice 4-5 weeks of age. In older mice there was an apparent thinning of body hair in general, and a luster-less appearance of the coat. On the back the skin surface was sometimes covered with fine scales. From the age of 5-6 weeks and onwards several of these transgenic animals showed signs of itch with scratching, the frequency of which increased with time.

Diagnostic necropsies with routine histological analyses were carried out on transgenic mice of the #1010 and #107 C57BL/6JxCBA lines, and of littermate controls. Tissues examined were brain, cerebellum, intestines (duodenum/jejunum, ileum, colon, rectum), and skin. In some animals 3 weeks of age heart, liver, lung, salivary gland, spleen, thymus and thyroid were also examined. In littermate controls (for #1010: 3 weeks, n = 5; 5 weeks, n = 5; for #107 5 weeks, n = 3) and transgenic mice of the #107 line (5 weeks n = 3) no significant macro- or microscopic abnormalities were observed. In transgenic animals from line #1010 abnormalities were found in the skin, but in no other organs or tissues. In mice 3 weeks of age (*i.e.* before phenotypic changes could be observed by inspection of living animals) skin changes were found in all animals examined (n = 4). These changes included mild to moderate epidermal hyperplasia and hyperkeratosis and a mild cellular inflammatory reaction with mixed leukocytes in the upper dermis. In animals 5 weeks of age (n = 4) the skin abnormalities were of the same type but more pronounced with a marked acanthosis-like hyperplasia and a hyperkeratosis of the epidermis which was mainly orthokeratotic. In addition, the number of mast cells in the dermis was increased in some of the animals. Leukocyte invasion of the epidermis was occasionally found and then manifested as small groups of granulocytes within the thickened cornified layer, which at these sites was parakeratotic.

EXAMPLE 3.

Determining the expression of scce-mRNA, SCCE protein in mice and catalytically active SCCE in SV40e-scce-transgenic mice.

Isolation of tissues.

Tissue specimens were collected at different ages and immediately frozen and stored in liquid nitrogen until analyzed.

RNA Isolation and cDNA synthesis and Real Time Quantitative PCR.

From 50-300 mg of the isolated tissues liver, skin, lung, brain, small intestine, colon, and ear, total RNA were prepared using RNA STAT-60™ (Tel-Test "B", Inc., Friendswood,TX, USA) according to the manufacturer. 50µg of each RNA preparation were DNase treated using RQ1 DNase (Promega, Madison, WI, USA) according to Ausubel et al . About 1,6 µg total RNA from each tissue was used for cDNA synthesis. Three RNA samples from animals with same genetic background and tissue were mixed and cDNA synthesis was made using Superscript™ Preamplification System for First Strand cDNA Synthesis (Life Technologies, Inc. Gaithersburg, MD, USA) according to the manufacturer. The cDNA synthesis was primed using Oligo $d(T)_{12-18}$ primer. The synthesized cDNA were diluted 100x in water prior to real time quantification. Real time quantification was performed three times on each cDNA. Primer and probe for real time quantification of transgenic human SCCE were designed over exons four and five where the sequence between human and murine SCCE show little (less) homology. The forward primer (5'-GCGAACCCCCTGGAACAA-3') (SEQ ID NO: 28) covers the position 427 – 444 of the human cDNA sequence (ref. Hansson et al) in exon four. The reverse primer (5'-ACATCCACGCACATGAGGTCA-3') (SEQ ID NO: 29) covers the position 490 – 510 of the human cDNA sequence in exon five. The real time amplification probe (5'- CCTGTACTGTCTCCGGCTGGGGCACTACC- 3') (SEQ ID NO: 30) covers the position 445 – 473 of the human cDNA sequence in exon four, and was labelled with the reporter fluorescent dye FAM in the 5'- end and the quencher fluorescent dye TAMRA in the 3'-end. The amplification of PCR products and real time detection were performed in ABI Prism 7700 Sequence Detection System (PE Applied Biosystems, Foster City CA, USA). Amplification of a part of murine acidic ribosomal phosphoprotein P0 (ACC# X15267) was used as endogenous control for the real time quantitation studies. The relative quantitation was calculated according to the formula $2^{-\Delta\Delta T}$, where ΔC_T is the difference in C_T values between the target and the endogenous control (User Bulletin #2, PE Applied Biosystem).

SCCE-specific polyclonal antibodies.

Polyclonal antibodies to recombinant human SCCE were prepared and affinity purified as described by Sondell et al.(Sondell et al. 1996). These antibodies are reactive towards human SCCE and pro-SCCE, as well as murine SCCE.

Tissue preparation, ELISA, immunoblotting and zymography.

Tissue extracts for ELISA were prepared by homogenization of 200-400 mg frozen tissue in 1 ml dH_2O containing a mixture of protease inhibitors (Complete TM Protease Inhibitor

Cocktail Tablets cat. no. 1836153, Boehringer Mannheim, Germany), followed by centrifuging at 20 000 x g for 30 min at 4° C. Protein concentrations was determined by reaction with bicinchoninic acid with bovine serum albumin as standard

For SDS-polyacrylamide gel electrophoresis approximately 0.1 mg of mouse skin was homogenized in 10 ml of 1 M acetic acid and extracted over night at 4 °C. After clearing by centrifugation extracts were aliquoted, lyophilized, and resolubilized in electrophoresis sample buffer for zymography. SDS-polyacrylamide gel electrophoresis, zymography, and immunoblotting were carried out as described (Ekholm et al. 2000).

For ELISA polystyrene microtiter plates were coated with 100 µl of SCCE-specific rabbit polyclonal antibodies at a concentration of 7 µg/ml prepared in coating buffer (0.1 M Na_2CO_3, 0.02 % NaN_3 (w/v), pH 9.6). After incubation over night at 4°C on a wobbling table, the plate was washed once with washing buffer (10 mM NaH_2PO_4, 0.15 M NaCl, 0.05% (v/v) Tween 20, pH 7.2). Thereafter, 200 µl blocking buffer (10 mM NaH_2PO_4, 0.15 M NaCl, 0.1% (w/v) Bovine Serum Albumine (BSA), pH 7.2) was added to each well and the plate was incubated at 37 °C for 1h. The plate was washed three times with washing buffer, 50 µl of sample (or standard) in dilution buffer (10 mM NaH_2PO_4, 0.15 M NaCl, 0.1% (w/v) BSA, 0.05% (v/v) Tween 20, pH 7.2) was added to each well and the plate was incubated for 1h at 37 °C. Plates were washed three times with washing buffer, and further prepared by adding 100 µl/well of SCCE-specific antibodies (7 µg/ml) labelled with alkaline phosphatatse Plates were incubated for 1h at 37 °C before washing three times with washing buffer. Development was performed by addition of 100 µl freshly prepared substrate solution (2 tablets of phosphatase substrate (Sigma104 phosphatase substrate tablets) dissolved in 10 ml 0.1 diethanol amine-HCl, 0.5mM $MgCl_2$, pH 9.8). Plates were incubated in the dark for 30 min at room temperature. Finally, 25 µl stop solution was added to each well and the absorbance was read at 405 nm. For quantitation recombinant human pro-SCCE (Hansson et al) was used as standard.

RESULTS

Real Time Quantification of human SCCE transcribed in transgenic mice.

In order to investigate if the difference in skin phenotype between #1010 ABD #107 transgenic lines expression of *hscce* mRNA in various tissues was analyzed by quantitative RT-PCR. The results are shown in Fig. 3A.

Six different tissues were analyzed. The analyses showed significantly higher expression of *hscce* in all tissues examined for transgenic mice of the #1010 line as compared to mice of the #107 line and non-transgenic littermates. The highest relative *hscce* mRNA levels were found in the intestines and lungs, but the difference in *hscce* expression between the two transgenic lines was most pronounced for skin, in which the relative level of *hscce* mRNA was about 24 times higher in #1010 mice than in #107 mice.

ELISA

Analyses of SCCE protein with ELISA (Fig. 4B) showed values close to or below the detection limit for tissues from transgenics of the #107 line and normal controls. In #1010 transgenics SCCE protein was readily detectable in several tissues including skin, intestines, and lung, the relative level (ng/mg) being highest in the skin.

Immunoblotting and zymography

Immunoblotting with SCCE-specific antibodies corroborated the ELISA-results. In extracts of skin of control mice small amounts of a component with molecular mass similar to human SCCE was detected, whereas a component with the same relative molecular mass detected in high amounts in skin extracts from #1010 transgenic mice (Fig. 4A). Zymography in casein-containing acrylamide gels showed that the extracts of skin from #1010 transgenics contained a proteolytic enzyme with the same electrophoretic mobility as human SCCE. A corresponding enzyme could not be detected in control extracts (Fig. 4B; the amounts of active murine SCCE are too low to be detected under the experimental conditions used). These results suggest that a fraction of the human pro-SCCE produced in skin of #1010 transgenics is converted to proteolytically active enzyme. This was supported also by the immunoblotting experiments (Fig. 3A), where a component corresponding to active human SCCE was labelled with the antibodies. In addition to SCCE, the skin extracts of #1010 transgenics contained increased amounts of a proteolytic enzyme not related to SCCE. The nature of this enzyme is presently not known.

CONCLUSION

The expression of *hscce* in various tissues at the RNA level was higher in #1010 transgenic mice than in the #A107 transgenic mice. The difference between transgenics from the two lines was even more pronounced as regards expression of SCCE-protein. In skin of #1010

transgenic mice high amounts of SCCE protein could be detected with immunoblotting. The majority of this protein appeared to be pro-SCCE, but also active SCCE could be detected in increased amounts.

EXAMPLE 4

Scce-transgenic mice as models for studies of inflammatory skin diseases and itch

Three male transgenic #1010 mice were mated with wild type C57BL/6J females, resulting in 6 litters with a total of 40 mice. Of these 19 (8 transgenics) were sacrificed at the age of 7-8 weeks and 21 (11 transgenics) were followed to the age of 13-14 weeks. In the latter group scratch movements with the legs were quantified.

Macroscopic phenotypic changes in transgenic #1010 animals were noted as a loss of hair from a narrow zone around the eyes in mice 4-5 weeks of age. In older mice there was an apparent thinning of body hair in general, and a luster-less appearance of the coat. On the back the skin surface was sometimes covered with fine scales. From the age of 5-6 weeks and onwards several of these transgenic animals showed signs of itch with scratching, the frequency of which increased with time.

Itching behavior

Of the 11 transgenic mice followed for 13-14 weeks 8 animals (73%) showed signs of itch (at least one period of scratching with hind or fore paws per minute) at the age of 10-11 weeks. The frequency of scratching varied among the observed animals; whereas some animals showed weak or moderate signs of itch, other animals spent most of their time scratching (Fig. 5). Up to the age of 3 weeks there was no statistically significant difference in weight between transgenic and normal animals. With increasing age there was a tendency towards lower weights among transgenics. At the age of 14-15 weeks there was a 7-10% reduction in weight in transgenics as compared to wild-type litter mates (mean for males 27.0 gm versus 30.0 gm; $p = 0.022$; mean for females 21.7 gm versus 23.5 gm; $p = 0.033$).

Histological analysis

For histology and immunohistochemistry (Ekholm et al. 1998 and Sondell et al. 1996) samples were either formaldehyde fixed and paraffin embedded according to routine protocols or frozen after fixation for 2 h in formaldehyde.

Upon sacrifice of the animals tissues (dorsal skin, large and small intestines, and lung) were prepared for microscopic analyses. The preliminary microscopic examination of routinely processed skin samples was carried out blindly (the examiner was not informed

about genotype or scratching behavior). In all cases but one, transgenics could be differed from wild type controls, the most prominent difference being the thickened epidermis in transgenic animals. Epidermal thickness was 55 µm (SD = 21 µm; n = 19) for transgenic animals, and 15 µm (SD = 2.6 µm; n = 21; $p < 0.001$) for controls. There was no statistically significant difference in epidermal thickness between younger (7 – 8 weeks) and older (13-14 weeks) transgenic animals. Other prominent and frequent histological findings in skin of transgenic animals as compared to controls (Fig. 6 A-B) were a marked hyperkeratosis, an increased cellularity of the dermal part of the skin, and increased epithelial thickness of adnexal structures (hair follicle walls and sebaceous glands and ducts). The increase in number of cells in the connective tissue was only partially due to lymphocytes and granulocytes; there appeared to be an increase also in the number of fibroblasts and/or histiocyte-like cells. Tolouidine blue staining showed increased number of dermal mast cells in some transgenic animals (results not shown). In routine stained sections no differences could be found between transgenics and controls for any of the other organs examined (results not shown).

Immunohistochemistry

Immunohistologic analyses of skin samples from #1010 transgenic animals and littermate controls with SCCE-specific antibodies showed strong labelling of keratinocytes in suprabasal parts of interfollicular epidermis in transgenics, including the thickened cornified layer. In hair follicles and sebaceous ducts only luminal parts, including the cornified lining of follicles and ducts, were stained (Fig. 6C). This was in marked contrast to basal cells of interfollicular epidermis and the major parts of hair follicles and sebaceous ducts and glands, where no or very weak labelling by the antibodies was seen. In controls there was a relatively weak labelling of a narrow zone of interfollicular epidermis close to the transition to the stratum corneum, of the stratum corneum, and of luminal parts of hair follicles (Fig. 6D). This pattern was similar to that previously described for normal human epidermis (Ekholm et al 1998). With immunofluorescence microscopy on formaldehyde fixed frozen samples similar results (not shown) were obtained.

In the intestines SCCE-specific labelling was seen only in transgenics and in irregularly distributed epithelial cells. Stained cells were more numerous at the tips of villi in the small intestine and in the luminal parts of colonic epithelium. In the lungs of transgenics apical parts of bronchiolar epithelia cells were weakly labelled. At higher antibody concentrations there appeared to be a diffuse labelling also of the alveolar epithelium (results for intestines and lung not shown).

Comparison with diseased human skin.

Skin biopsies from human volunteers and patients were taken after informed consent and with the approval of the Human research ethics committee, Umeå University. Biopsies were taken from chronic eczematous lesions on the flexural sides of lower arms of five adults with atopic dermatitis and processed for microscopy as above. Biopsies from corresponding sites were obtained from volunteers. In routine stained sections (not shown) the lesions showed, as expected, marked acanthosis, hyperkeratosis, and a sparse dermal infiltrate consisting mainly of lymphocytes. Immunohistology with SCCE-specific antibodies showed a drastic increase in the number of labelled suprabasal cell layers as compared to controls (Fig. 6 E-F). As regards the acanthosis, hyperkeratosis, and pattern of SCCE-specific staining the differences seen between lesional and normal skin were strikingly similar to those seen between skin of #1010 transgenic mice and controls.

EXAMPLE 5.

Scce-transgenic mice for testing of antipruritic agents

Transgenic mice, 18-22 weeks of age, mean weight 24.2 g, were given subcutaneous injections of either 250 µg of the glucocorticoid triamcinolone acetonide in a total volume of 100 µl on day 0, and 100 µg triamcinolone acetonide in a total volume of 100 µl on days 7, 14 and 21, or 100 µl of physiological saline at the same time points. Episodes of scratching were counted in the morning and injections were given in the afternoon. To prepare solutions for injections 25 µl or 10 µl or Kencort -T™ suspension, 10 mg/ml (Bristol-Myers Squibb), was mixed with 75 µl or 90 µl of physiological saline. The results are shown in Fig. 7. Triamcinolone acetonide was highly efficient in diminishing scratching.

Transgenic mice 20-21 weeks of age, mean weight 24.5 mg, were given either loratidine in a total volume of 100 µl, or 100 µl of a control solution by means of tube feeding. Episodes of scratching were counted immediately before feeding (0 hours), and then at time points as indicated. Feeding solutions were prepared by mixing either 30 µl of loratidine 1 mg/ml, sucrose 600 mg/ml (Clarityn mixture ™, Schering-Plough), or, for control solutions, 30 µl of sucrose 600 mg/ml, with 70 µl of physiological saline. The results are shown in Figure 8A. The same mice were then treated 7 days later with 90 µl of loratidine mixture of sucrose solution mixed with 10 µl of physiological saline. The results are shown in Figure 8B. As seen from figures 8A and 8B there was no significant difference in frequency of scratching between treatment group and control group. This indicates that the itching behavior of the SCCE mouse is not relieved by treatment with an antihistamine.

The two experiments show that *scce*-transgenic mice can be used for evaluation of drugs with potential effects on itch (anti-pruritic drugs). The glucocorticoid triamcinolone acetonide appeared to be highly effective in relieving itch, whereas the antihistamine loratidine had no statistically significant antipruritic effect.

It thus appears that the pruritus in SCCE-transgenic mice respond to treatment with a glucocorticoid but not to treatment with an antihistamine. A similar situation can be found for human patients suffering from pruritus associated with e.g. atopic dermatitis, eczema, and psoriasis.

EXAMPLE 6

Determination of nucleotide sequences of homologues to hscce-cDNA from cow, rat and pig.

Skin biopsies from cow, pig and rat were obtained, immediately frozen in liquid nitrogen and homogenized, using a Mikro-Dismembranator U (B.Braun Biotech International GmbH, Melsungen, Germany) at 2000 rpm for 45 s. RNA was isolated using 1ml of Trizol Reagent (Life Technologies AB, Täby, Sweden) according to the manufacturers instructions, DNase treated, extracted with Phenol:$CHCl_3$, and precipitated with LiCl according to the Boehringer Mannheim protocol (Nonradioactive In Situ Hybridization application Manual, Boehringer Mannheim, Mannheim, Germany).
RT-PCR was performed as described (Lindström *et al.* with oligo $d(T)_{16}$ primers (Perkin Elmer, Foster City, CA, USA) in the RT reaction. In each RT reaction 100 ng of total RNA was used.

For PCR five primers were designed from conserved sequences found in *hscce* and *mscce* cDNA resulting in primers mS3, 698,696,H2 and mS4 (Table 4). PCR products were cloned into pCR II vector using the TOPO TA cloning kit (Invitrogen/NOVEX, Groeningen, The Netherlands) as recommended by the manufacturers. Plasmid DNA was isolated using the QIAprep Spin Miniprep Kit (Qiagen, Chatsworth, CA). Nucleotide sequencing was performed using the DYEnamic ET Terminator Cycle Sequencing Kit (Amersham Pharmacia Biotech Sverige, Uppsala, Sweden) and an ABI377 automated DNA sequencer (Perkin-Elmer).

To obtain the 5´cDNA end the SMART Race cDNA Amplification Kit (Clontech Laboratories,Inc., Palo Alto, Ca) was used according to the manufacturers instructions. Species specific primers were designed from the cDNA sequences obtained in previous steps (Table 4).

Table 4. Oligomer primers used in RT-PCR, 5´-RACE and nested 5´-RACE
Oligomers a – e were designed from conserved sequences found when comparing SCCE and mSCCE cDNA sequences. Positions are derived from the mSCCE cDNA(Bäckman et al., Oligomers f – j were designed based on nucleotide sequencing data from the preceding species specific cloning reactions.

Oligomer	Sequence, 5´ to 3´	
a) mS3	CAAGGAGAAAGGATTATAGATGGCT	(SEQ ID NO: 31)
b) 698	AAGGCTCCGCACCCATGGCAG	(SEQ ID NO: 32)
c) 696	TGCAATGGTGACTCAGGGGGGCCCTT	(SEQ ID NO: 33)
d) H2	GACCCAGGCGTCTACACTCAAGT	(SEQ ID NO: 34)
e) mS4	GAGACCATGAAAACCCATCGCTAAC	(SEQ ID NO: 35)
f) KO0905	TGACTTTCTTCACACTGGACGACAGC	(SEQ ID NO: 36)
g) GR0905	CTTCACACTGGCTGATAGCCTGGCCG	(SEQ ID NO: 37)
h) Ngr	CAGGGTGGCGGAATGACCTCATGGCCCT	(SEQ ID NO: 38)
i) RÅ1016	CTACTCCACAAGGACCCATGTCAATGAC	(SEQ ID NO: 39)
j) nRÅ1016	GCTGTGTGCTGGCATTCCCGACTCTAAG	(SEQ ID NO: 40)

First strand cDNA was prepared from total RNA using SMART II oligonucleotide (5´-AAGCAGTGGTAACAACGCAGAGTACGCGGG-3´) (SEQ ID NO: 41) and 5´-RACE cDNA synthesis primer (5´-$(T)_{25}$ N_{-1}N-3´) (N = A, C, G, or T; N_{-1} = A, G, or C) (SEQ ID NO: 42). 5´-RACE was performed using Universal primer mix (UPM) containing Long (0.02μM) (5´-CTAATACGACTCACTATAGGGCAAGCAGTGGTAACAACGCAGAGT-3´) (SEQ ID NO: 43) and Short (1μM) (5´-CTAATACGACTCACTATAGGGCC-3´) (SEQ ID NO: 44) universal primer and a specific primer for each species (KO 0905, GR 0905 and RÅ 1016). Cyclic parameters for the PCR reaction were adapted from the manufacturers recommendations for a Perkin-Elmer DNA Thermal Cycler 480 but with 25 cycles in the last step. 5´-RACE PCR products from reactions with specific primers for pig and rat were subjected to nested PCR using Nested Universal Primer (NUP) (5´-AAGCAGTGGTAACAACGCAGAGT-3´) (SEQ ID NO: 45) and nested specific primers for pig (nGR0905) and rat (nRÅ1016) respectively. The nested PCR reactions were performed according to the manufacturers instructions with 20 cycles of amplification. Products from 5´-RACE and nested 5´-RACE were checked on agarose gel. For characterization products were cloned and sequenced as described above. The results are shown in table 5 as deduced amino acid sequences. Table 6 show the calculated similarities of the active enzyme starting with the sequence IIDG. Sequences for human (Hansson et al., 1994) and mouse SCCE (Bäckman et al., 1999) are included for comparison.

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The rat SCCE sequence shown in table 5 and in SEQ ID NO: 49 can not be found in the GenBank database which indicate that it does not correspond to any of the already known rat kallikreins or kallikrein like proteins.

Table 5. Alignment of the deduced amino acid sequences of SCCE from five species. The sequences for cow, pig, and rat are not complete in the C-terminal parts.

```
seq2  ----MTTPLVILLLTFALGSVA QEDQGNKSGEKIIDGVPCPRGSQPWQVALLKGSQLHCG 56
seq3  MARPLLPPRLILLLSLALGSAA QEGQ-DKSGEKIIDGVPCPGGSRPWQVALLKGNQLHCG 59
seq1  MARSLLLPLQILLLSLALETAG EEAQ----GDKIIDGAPCARGSHPWQVALLSGNQLHCG 56
seq4  -MGVWLLSLLTVLLSLALETAG Q-------GERIIDGYKCKEGSHPWQVALLKGDQLHCG 52
seq5  -MGVWLLSLITVLLSLALETAG Q-------GERIIDGIKCKEGSHPWQVALLKGNQLHCG 52

seq2  GVLLNEQWVLTAAHCMN-EYNVHMGSVRLVGG--QKIKATRSFRHPGYSTQTHANDLMLV 112
seq3  GVLVNQQWVLTAAHCMMNDYNVHLGSDRLDDRKGQKIRAMRSFRHPGYSTQTHANDLMLV 112
seq1  GVLVNERWVLTAAHCKMNEYTVHLGSDTLGDRRAQRIKASKSFRHPGYSTQTHVNDLMLV 119
seq4  GVLVGESWVLTAAHCKMGQYTVHLGSDKIEDQSAQRIKASRSFRHPGYSTQTHVNDLMLV 116
seq5  GVLVDKYWVLTAAHCKMGQYQVQLGSDKIGDQSAQKIKATKSFRHPGYSTKTHVNDIMLV 112

seq2  KLNGRAKLSSSVKKVNLPSHCDPPGTMCTVSGWGTTTSPDVTFPGQLMCTDVKLISPQDC 172
seq3  KLSRPARLSASVKKVNLPSRCEPPGTTCTVSGWGTTTSPDVTFPADLMCTDVKLISSQDC 179
seq1  KLNSQARLSSMVKKVRLPSRCEPPGTTCTVSGWGTTTSPDVTFPSDLMCVDVKLISPQDC 176
seq4  KMDKPVKMSDKVQKVKLPDHCEPPGTLCTVSGWGTTTSPDVTFPSDLMCSDVKLISSQEC 171
seq5  RLDEPVKMSSKVEAVQLPEHCEPPGTSCTVSGWGTTTSPDVTFPSDLMCSDVKLISSREC 172

seq2  RKVYKDLLGDSMLCAGIPNSRTNACNGDSGGPLMCKGTLQGVVSWGSFPCGQPNDPGVYT 232
seq3  KKVYKDLLGSSMLCAGIPNSKTNACNGDSGGPLVCKGTLQGLVSWGTFPCGQPNDPGVYT 239
seq1  TKVYKDLLENSMLCAGIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTFPCGQPNDPGVYT 236
seq4  KKVYKDLLGKTMLCAGIPDSKTNTCNGDSGGPLVCNDTLQGLVSWGTYPCGQPN------ 225
seq5  KKVYKDLLGKTMLCAGIPDSKTNTCNGDSGGPLVCNDTLQGLASRGTYPCGQPNDPGVYT 232

seq2  QVCKYVNWIK------- 242
seq3  QVCKYIDWIN------- 249
seq1  QVCKFTKWINDTMKKHR 253
seq4  ----------------
seq5  QVCKYKRWVMETMKTHR 249
```

Seq 2 (cow) in the figure is SEQ ID NO:46, Seq 3 (pig) in the figure is SEQ ID NO:47, Seq 1 (homo) in the figure is SEQ ID NO:48, Seq 4 (rat) in the figure is SEQ ID NO:49 and Seq 5 (mouse) in the figure SEQ ID NO:50.

Table 6. Calculated similarities of the active enzymes.

species compared	calculated similarity *
Mouse-human	75%
Rat-human	77%
Pig-human	77%
Cow-human	76%
Rat-mouse	88%
Cow-mouse	69%
Pig-mouse	69%

*The comparisons of active enzymes are starting with the sequence IIDG etc.

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